WHAT IS CLAIMED IS:

- 1. A material having a fluorogenic moiety linked to a solid support,
- 2 said material having the structure:

4 wherein:

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R¹, R², R³, R⁴, R⁵ and R⁶ are members independently selected from the group consisting of H, halogen, -NO₂, -CN, -C(O)_mR⁷, -C(O)NR⁸R⁹, -S(O)_tR¹⁰, -SO₂NR¹¹R¹², -OR¹³, substituted or unsubstituted alkyl, -R¹⁴-SS, and -NHR¹⁵ with the proviso that at least one of R¹, R², R³, R⁴, R⁵ and R⁶ is -R¹⁴-SS and at least one of R¹, R², R³, R⁴, R⁵ and R⁶ is -NHR¹⁵,

wherein:

11 R⁷, R⁸, R⁹, R¹⁰, R¹¹, R¹² and R¹³ are members independently

12 selected from the group consisting of H, substituted or

13 unsubstituted alkyl and substituted or unsubstituted aryl;

14 R¹⁴ is a linking group adjoining said fluorogenic moiety and said

15 solid support;

16 R¹⁵ is a member selected from the group consisting of amine

R¹³ is a member selected from the group consisting of amine protecting groups, -C(O)-AA and -C(O)-P:

18 wherein:

P is a peptide sequence;

AA is an amino acid residue;

21 m is a member selected from the group consisting of the integers 1
22 and 2;

23 t is a member selected from the group consisting of the integers 24 from 0 to 2; and

25 SS is a solid support.

2. The material according to claim 1, wherein said linking group is a member selected from the group consisting of substituted or unsubstituted alkyl, substituted or unsubstituted heteroalkyl and substituted or unsubstituted aryl;

The material according to claim 1, wherein P is a peptide sequence comprising the structure:

wherein,

AA¹-AA²-(AA¹)_{J-2} is a peptide sequence, wherein each of AA¹ through

AA¹ is an amino acid residue which is a member independently

selected from the group of natural amino acid residues, unnatural

amino acid residues and modified amino acid residues;

J denotes the number of amino acid residues forming said peptide sequence and is a member selected from the group consisting of the numbers from 2 to 10, such that J-2 is the number of amino acid residues in the peptide sequence exclusive of AA¹-AA²; and

i denotes the position of said amino acid residue relevant to AA^1 and when J is greater than 2, i is a member selected from the group consisting of the numbers from 3 to 10.

4. The material according to claim 1, wherein R¹⁵ has the structure:
-C(O)-AA; and

AA is an amino acid residue selected from the group consisting of natural amino acids, unnatural amino acids and modified amino acids.

5. The material according to claim 1, having the structure:

6. The material according to claim 5, having the structure:

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wherein, Z is a member selected from the group consisting of -O-, and $-NR^{16}$ -; and

4 -NR

c is a member selected from the integers from 0 to 6.

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7. A material according to claim 6, having the structure:

$$O \longrightarrow R^{1} \longrightarrow NHC(O)AA^{1} \longrightarrow AA^{2} \longrightarrow (AA^{i})_{J-2}$$

$$O \longrightarrow R^{3}$$

$$O \longrightarrow R^{4}$$

$$SS$$

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- 8. A method of assaying for the presence of an enzymatically active protease in a sample, said method comprising:
 - (a) contacting said sample with a material according to claim 3 in such a manner whereby said fluorogenic moiety is released from said peptide sequence upon action of said protease, thereby producing a fluorescent moiety; and
- (b) observing whether said sample undergoes a detectable change in fluorescence, said detectable change being an indication of the presence of said enzymatically active protease in said sample.
- 1 9. The method according to claim 8, wherein said protease is a 2 member selected from the group consisting of aspartic protease, cysteine protease, 3 metalloprotease and serine protease.
- 1 10. The method according to claim 8, wherein said protease is a 2 protease of a microorganism.

1	11.	The method according to claim 10, wherein said microorganism is
2	a member selected from	n the group consisting of bacteria, fungi, yeast, viruses, and
3	protozoa.	
	•	
1	12.	The method according to claim 8, wherein said sample is a clinical
2	sample from a subject.	
1	13.	The method according to claim 8, further comprising (c)
2	quantifying said fluore	escent moiety, thereby quantifying said protease.
	-	
1		A method of assaying for the presence of a selected microorganism
2	in a sample by probing	g the sequence specificity of peptide cleavage by a protease of said
3	microorganism, said n	
4	(a) con	tacting a sample suspected of containing said selected
5		microorganism with a material according to claim 3, wherein said
6		peptide comprises a sequence that is selectively cleaved by said
7		protease of said selected microorganism, thereby releasing the
8		fluorogenic moiety from the peptide sequence;
9	(b) det	ecting the cleavage by detecting fluorescence arising from a
10		fluorescent moiety produced by cleavage of said fluorogenic
11		moiety from said peptide sequence, thereby confirming said
12		presence of said selected microorganism in said sample.
		The method according to claim 14, further comprising (c)
1	15.	
2	quantifying said fluor	rescence, thereby quantifying said protease of said microorganism.
1	16.	A fluorogenic peptide comprising a fluorogenic moiety covalently
2	bound to a peptide se	equence, said peptide having the structure:
3		R-P
4	wherein:	
5	_	peptide sequence having the structure:
6		$-C(O)-AA^{1}-AA^{2}-(AA^{i})_{J-2}$
-		
7	wherein:	

each of AA1 through AAi is an amino acid residue which is a member 8 independently selected from the group of natural amino acid 9 residues, unnatural amino acid residues and modified amino acid 10 residues; 11 J denotes the number of amino acid residues forming said peptide 12 sequence and is a member selected from the group 13 consisting of the numbers from 2 to 10, such that J-2 is the 14 number of amino acid residues in the peptide sequence 15 exclusive of AA¹-AA²; 16 i denotes the position of said amino acid residue in sequence 17 relative to AA^1 and when J is greater than 2, i is a member 18 selected from the group consisting of the numbers from 3 to 19 10; and 20 R is a fluorogenic moiety having the structure: 21 22 23 wherein: R¹, R², R³, R⁴, R⁵ and R⁶ are members independently selected from the 24 group consisting of H, halogen, -NO2, -CN, 25 $-C(O)_{m}R^{6}$, $-C(O)NR^{7}R^{8}$, $-S(O)_{t}R^{9}$, $-SO_{2}NR^{10}R^{11}$, $-OR^{12}$, substituted 26 or unsubstituted alkyl, -NHC(O)-P, and -R²⁰-Y, with the proviso 27 that at least one of R^1 , R^2 , R^3 , R^4 , R^5 and R^6 is $-R^{20}$ -Y and at least 28 one of R¹, R², R³, R⁴, R⁵ and R⁶ is -NHC(O)-P, 29 wherein: 30 R⁶, R⁷, R⁸, R⁹, R¹⁰, R¹¹ and R¹² are members independently 31 selected from the group consisting of H, substituted or 32 unsubstituted alkyl and substituted or unsubstituted aryl; 33 R²⁰ is either present or absent and is a member selected from the 34 group consisting of substituted or unsubstituted alkyl and 35

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substituted or unsubstituted heteroalkyl;

- Y is a member selected from the group consisting of organic

 functional groups and methyl;

 m is a member selected from the group consisting of the integers 1

 and 2; and

 t is a member selected from the group consisting of the integers

 from 0 to 2.
 - 17. The fluorogenic peptide according to claim 16, wherein said
 2 organic functional group is a member selected from the group consisting of -COOR¹⁷,
 3 CONR¹⁷R²¹, -C(O)R¹⁷R²¹, -OR¹⁷, -SR¹⁷, -C(O)SR¹⁷ and -NR¹⁷R²¹
 4 wherein, R¹⁷ and R²¹ are members independently selected from H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl.
 - 18. A fluorogenic peptide according to claim 16, having the structure:

$$O \longrightarrow O \longrightarrow NHC(O)AA^{1} - AA^{2} - (AA^{i})_{J-2}$$

$$R^{6} \longrightarrow R^{5} \qquad R^{4}$$

19. A fluorogenic peptide according to claim 18, having the structure:

$$O \longrightarrow O \longrightarrow NHC(O)AA^1 \longrightarrow AA^2 \longrightarrow (AA^i)_{J-2}$$

$$R^3$$

$$R^4$$

3 wherein:

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c is a member selected from the group consisting of the integers from 0 to 6.

20. A fluorogenic peptide according to claim 19, having the structure:

1	21.	The fluorogenic peptide according to claim 16, wherein said
2	peptide sequence com	prises a peptide bond that is cleaved by a protease releasing said
3	fluorogenic moiety from said peptide sequence, thereby producing a fluorescent moiety	
4	and a peptide moiety.	
_	22	The fluorogenic peptide according to claim 21, wherein said
1	22.	
2		ed between a carboxyl of the carboxy-terminus amino acid residue
3	and an amine group of	of said fluorogenic moiety.
1	23.	A method of assaying for the presence of an enzymatically active
2		said method comprising:
3		ntacting a sample suspected of containing said protease with a
4	peptide according to claim 16 in such a manner whereby said fluorogenic moiety is	
5	released from said peptide sequence upon action of said protease, thereby producing a	
6	fluorescent moiety; and	
7	(b) ob	serving whether said sample undergoes a detectable change in
8	fluorescence, said detectable change being an indication of the presence of said	
9		protease in said sample.
1	24.	The method according to claim 23, wherein said protease is a
2	member selected fro	om the group consisting of aspartic protease, cysteine protease,
3		
	25.	The method according to claim 23, wherein said protease is a
1		
2	protease of a microo	organism.
1	26.	The method according to claim 25, wherein said microorganism is
2	the state of the storie funcions and	
3	protozoa.	
		The state of the s
1	27.	The method according to claim 23, wherein said sample is a
2	clinical sample from	n a subject.
1	28.	The method according to claim 27, wherein said subject is a
2	human.	

1	29.	The method according to claim 23, further comprising (c)
2	quantifying said fluore	escent moiety, thereby quantifying said protease.
1	30.	A method of assaying for the presence of a selected microorganism
2		g the sequence specificity of peptide cleavage by a protease of said
3	microorganism, said n	
4		tacting a sample suspected of containing said selected
5	, ,	microorganism with a material according to claim 16, wherein said
6		peptide comprises a sequence that is selectively cleaved by a
7		protease of a selected microorganism, thereby releasing said
8		fluorogenic moiety from said peptide sequence;
9	(b) det	ecting said cleavage by detecting fluorescence arising from a
10		fluorescent moiety produced by cleavage of said fluorogenic
11		moiety from said peptide sequence, thereby confirming said
12		presence of said selected microorganism in said sample.
1	31.	The method according to claim 30, further comprising (c)
2		rescence, thereby quantifying said protease of said microorganism.
1	32.	A library of fluorogenic peptides comprising at least a first peptide
2		sequence covalently attached to a first fluorogenic moiety and a
3		g a second peptide sequence covalently attached to a second
4		said first peptide and said second peptide having the structure:
		R-P
5		IX-1
6	wherein:	
7		aid first peptide and said second peptide, P is independently selected
8	from	peptide sequences having the structure:
9		$-C(O)-AA^1-AA^2-(AA^i)_{J-2}$
10	wherein:	
11	each	of AA ¹ through AA ⁱ is an amino acid residue which is a member
12		independently selected from the group consisting of natural amino
13		acid residues, unnatural amino acid residues and modified amino
14		acid residues;

each J is independently selected and denotes the number of amino acid 15 residues forming said first peptide sequence and said second 16 peptide sequence and is a member selected from the group 17 consisting of the numbers from 2 to 10; 18 each i is independently selected and denotes the position of said amino 19 acid residue relative to AA^1 and when J is greater than 2, i is a 20 member selected from the group consisting of the numbers from 3 21 to 10; and 22 for each of said first peptide and said second peptide R is independently selected 23 from fluorogenic moieties having the structure: 24 25 wherein: 26 R¹, R², R³, R⁴, R⁵, and R⁶ are members independently selected from the 27 group consisting of H, halogen, -NO₂, -CN, -C(O)_mR⁷, 28 -C(O)NR⁸R⁹, -S(O)_tR¹⁰, -SO₂NR¹¹R¹², -OR¹³, substituted or 29 unsubstituted alkyl, -NH-C(O)-P, R²⁰-Y and -R¹⁴-SS, with the 30 proviso that for each peptide at least one of R¹, R², R³, R⁴ and R⁵ is 31 a member independently selected from -R¹⁴-SS and R²⁰-Y and at 32 least one of R¹, R², R³, R⁴, R⁵, and R⁶ is -NH-C(O)-P, 33 wherein: 34 R⁷, R⁸, R⁹, R¹⁰, R¹¹, R¹² and R¹³ are members independently 35 selected from the group consisting of H, substituted or 36 unsubstituted alkyl and substituted or unsubstituted aryl; 37 R¹⁴ is a linking group adjoining said fluorogenic moiety and the 38 solid support; 39 R²⁰ is either present or absent and is a member selected from the

functional groups and methyl;

substituted or unsubstituted heteroalkyl;

Y is a member selected from the group consisting of organic

group consisting of substituted or unsubstituted alkyl and

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	m is a member selected from the group consisting of the integers
45	m is a illemoof scienced from the
46	from 1 to 2;
47	t is a member selected from the group consisting of the integers
48	from 0 to 2;
49	Y is a member selected from the group consisting of -COOR ¹⁷ ,
50	$CONHR^{17}$, $-C(O)R^{17}$, $-OR^{17}$, $-SR^{17}$, and NHR^{17} ;
51	R ¹⁷ is a member selected from the group consisting of H,
	substituted or unsubstituted alkyl and substituted or
52	
53	unsubstituted aryl; and
54	SS is a solid support.
	1 1 inline group is

- The library according to claim 32, wherein said linking group is a 33. 1 member selected from the group consisting of substituted or unsubstituted alkyl and 2 substituted or unsubstituted heteroalkyl 3
- The library according to claim 32, wherein said organic functional 34. 1 group is a member selected from the group consisting of -COOR¹⁷, CONR¹⁷R²¹, 2 -C(O) $R^{17}R^{21}$, -O R^{17} , -S R^{17} , -C(O)S R^{17} , and -N $R^{17}R^{21}$ 3 wherein, R¹⁷ and R²¹ are members independently selected from H, 4 substituted or unsubstituted alkyl and substituted or unsubstituted aryl. 5
- The library of fluorogenic peptides according to claim 32, wherein 35. 1 R-P has the structure: 2

A library of fluorogenic peptides according to claim 35, wherein 36. 1

R-P has the structure: 2

$$O \longrightarrow R^1$$

$$NHC(O)AA^1 - AA^2 - (AA^i)_{J-2}$$

$$R^3$$

34 wherein,

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c is a member selected from the group consisting of the numbers from 0 to 6.

1 37. A library of fluorogenic peptides according to claim 36, wherein

2 R-P has the structure:

- 1 38. The library according to claim 32, wherein said fluorogenic moiety of said first peptide and said fluorogenic moiety of said second peptide are different
- 3 fluorogenic moieties.
- 1 39. The library according to claim 32, wherein said first peptide sequence are identical.
- 1 40. The library according to claim 32, wherein said first peptide 2 sequence and said second peptide sequence are different.
- 1 41. The library according to claim 40, wherein an amino acid residue
- 2 selected from the group consisting of AA¹, AA², AAⁱ and combinations thereof of said
- 3 first peptide is a different amino acid residue than an amino acid residue at a
- 4 corresponding position relative to AA¹ of said second peptide.
- 1 42. The library according to claim 32, wherein AA¹ of said first
- 2 peptide sequence and AA¹ of said second peptide sequence are identical amino acid
- 3 residues.

1 43. The library according to claim 32, wherein AA ¹ of said first 2 peptide sequence and AA ¹ of said second peptide sequence are different amino acid 3 residues. 1 44. The library according to claim 32, wherein AA ² of said first 2 peptide sequence and AA ² of said second peptide sequence are identical amino acid 3 residues. 1 45. The library according to claim 32, wherein AA ² of said first	
residues. 1 44. The library according to claim 32, wherein AA ² of said first peptide sequence and AA ² of said second peptide sequence are identical amino acid residues.	
1 44. The library according to claim 32, wherein AA ² of said first 2 peptide sequence and AA ² of said second peptide sequence are identical amino acid 3 residues.	
 peptide sequence and AA² of said second peptide sequence are identical amino acid residues. 	
3 residues.	
- 11 wherein AA^2 of said first	
The library according to claim 34, who our 12 2 3 3 3 3 3	
1 A A 2 of said accord pentide sequence are different amino acid	
3 residues.	
1 46. The library according to claim 32, wherein AA' of said first peptide	
2 sequence and AA ⁱ of said second peptide sequence are identical amino acid residues.	
y wherein A A ⁱ of said first peptide	;
The library according to claim 32, wherem 747 of said 2 sequence and AA ⁱ of said second peptide sequence are different amino acid residues.	
1 48. The library according to claim 42, comprising at least six peptides	
2 having different peptide sequences, wherein AA ¹ is a different amino acid residue in each	1
of said different peptide sequences.	
1: As alsim 48 comprising at least twelve	
1 49. The library according to claim 46, comprising at reasonable 2 peptides having different peptide sequences wherein AA ¹ is a different amino acid residu	ıe
2 peptides having different peptide sequences wherein 747 is a different peptide sequences.	
3 in each of said different peptide sequences.	
The library according to claim 49, comprising at least twenty	
2 peptides having different peptide sequences wherein AA ¹ is a different amino acid residu	ue
3 in each of said different peptide sequences.	
wherein AA ¹ is a member	
1 51. The library according to claim 32, wherein Art is a member of	
selected from the group consisting of Lys, Arg, Leu and combinations thereof.	
The library according to claim 32 , wherein J is a member selecte	d
2 from the numbers from 4 to 8.	

of said first peptide and said second peptide is cleavable by a protease into a fluorescent moiety and the peptide sequence. 54. The library according to claim 32, comprising at least 10 peptides, wherein each of the peptide sequences is a different peptide sequence. 55. The library according to claim 54, comprising at least 100 peptides, wherein each of the peptide sequences is a different peptide sequence. 56. The library according to claim 55, comprising at least 1,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 57. The library according to claim 56, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 58. The library according to claim 57, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 59. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 60. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. 61. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;	1	53. The library of peptides according to claim 32, wherein at least one
3 moiety and the peptide sequence. 1 54. The library according to claim 32, comprising at least 10 peptides, wherein each of the peptide sequences is a different peptide sequence. 1 55. The library according to claim 54, comprising at least 100 peptides, wherein each of the peptide sequences is a different peptide sequence. 1 56. The library according to claim 55, comprising at least 1,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 1 57. The library according to claim 56, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 1 58. The library according to claim 57, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 1 59. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 1 60. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. 1 61. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: 1 (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;	2	of said first peptide and said second peptide is cleavable by a protease into a fluorescent
wherein each of the peptide sequences is a different peptide sequence. 55. The library according to claim 54, comprising at least 100 peptides, wherein each of the peptide sequences is a different peptide sequence. 56. The library according to claim 55, comprising at least 1,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 57. The library according to claim 56, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 58. The library according to claim 57, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 59. The library according to claim 57, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 60. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 60. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. 61. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;		
wherein each of the peptide sequences is a different peptide sequence. The library according to claim 54, comprising at least 100 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 55, comprising at least 1,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 56, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 57, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 57, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. An elbod of determining a peptide sequence sequence is a different peptide is located at a second region of a substrate and said second peptide is located at a second region of a substrate. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;	5	
the library according to claim 54, comprising at least 100 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 55, comprising at least 1,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 56, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 57, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 58 comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;	1	
wherein each of the peptide sequences is a different peptide sequence. 56. The library according to claim 55, comprising at least 1,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 57. The library according to claim 56, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 58. The library according to claim 57, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 59. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 60. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. 61. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;	2	wherein each of the peptide sequences is a different peptide sequence.
wherein each of the peptide sequences is a different peptide sequence. 56. The library according to claim 55, comprising at least 1,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 57. The library according to claim 56, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 58. The library according to claim 57, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 59. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 60. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. 61. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;	_	The library according to claim 54, comprising at least 100 peptides,
1 56. The library according to claim 55, comprising at least 1,000 2 peptides, wherein each of the peptide sequences is a different peptide sequence. 1 57. The library according to claim 56, comprising at least 10,000 2 peptides, wherein each of the peptide sequences is a different peptide sequence. 1 58. The library according to claim 57, comprising at least 100,000 2 peptides, wherein each of the peptide sequences is a different peptide sequence. 1 59. The library according to claim 58 comprising at least 1,000,000 2 peptides, wherein each of the peptide sequences is a different peptide sequence. 1 60. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. 1 61. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: 1 (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;		
peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 56, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 57, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 60. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;	2	
peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 56, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 57, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 60. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. 61. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;	1	56. The library according to claim 55, comprising at least 1,000
57. The library according to claim 56, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 58. The library according to claim 57, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 59. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. 60. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. 61. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;		peptides, wherein each of the peptide sequences is a different peptide sequence.
peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 57, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;		
1 58. The library according to claim 57, comprising at least 100,000 2 peptides, wherein each of the peptide sequences is a different peptide sequence. 1 59. The library according to claim 58 comprising at least 1,000,000 2 peptides, wherein each of the peptide sequences is a different peptide sequence. 1 60. The library according to claim 32, wherein said first peptide is 2 located at a first region of a substrate and said second peptide is located at a second 3 region of a substrate. 1 61. A method of determining a peptide sequence specificity profile of 2 an enzymatically active protease, said method comprising: 3 (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released 5 from the peptide sequence, thereby forming a fluorescent moiety;	1	
peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;	2	peptides, wherein each of the peptide sequences is a different peptide sequence.
peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 58 comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;	1	The library according to claim 57, comprising at least 100,000
1 59. The library according to claim 58 comprising at least 1,000,000 2 peptides, wherein each of the peptide sequences is a different peptide sequence. 1 60. The library according to claim 32, wherein said first peptide is 2 located at a first region of a substrate and said second peptide is located at a second 3 region of a substrate. 1 61. A method of determining a peptide sequence specificity profile of 2 an enzymatically active protease, said method comprising: 3 (a) contacting said protease with a library of peptides according to claim 4 32 in such a manner whereby the fluorogenic moiety is released 5 from the peptide sequence, thereby forming a fluorescent moiety;		
peptides, wherein each of the peptide sequences is a different peptide sequence. 1 60. The library according to claim 32, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate. 1 61. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;	2	
1 60. The library according to claim 32, wherein said first peptide is 2 located at a first region of a substrate and said second peptide is located at a second 3 region of a substrate. 1 61. A method of determining a peptide sequence specificity profile of 2 an enzymatically active protease, said method comprising: 3 (a) contacting said protease with a library of peptides according to claim 4 32 in such a manner whereby the fluorogenic moiety is released 5 from the peptide sequence, thereby forming a fluorescent moiety;	1	
located at a first region of a substrate and said second peptide is located at a second region of a substrate. 61. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;	2	peptides, wherein each of the peptide sequences is a different peptide sequence.
located at a first region of a substrate and said second peptide is located at a second region of a substrate. 61. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising: (a) contacting said protease with a library of peptides according to claim 32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;		wherein said first pentide is
region of a substrate. 1 61. A method of determining a peptide sequence specificity profile of 2 an enzymatically active protease, said method comprising: 3 (a) contacting said protease with a library of peptides according to claim 4 32 in such a manner whereby the fluorogenic moiety is released 5 from the peptide sequence, thereby forming a fluorescent moiety;	1	
1 61. A method of determining a peptide sequence specificity profile of 2 an enzymatically active protease, said method comprising: 3 (a) contacting said protease with a library of peptides according to claim 4 32 in such a manner whereby the fluorogenic moiety is released 5 from the peptide sequence, thereby forming a fluorescent moiety;	2	located at a first region of a substrate and said second peptide is located at a second
2 an enzymatically active protease, said method comprising: 3 (a) contacting said protease with a library of peptides according to claim 4 32 in such a manner whereby the fluorogenic moiety is released 5 from the peptide sequence, thereby forming a fluorescent moiety;	3	region of a substrate.
2 an enzymatically active protease, said method comprising: 3 (a) contacting said protease with a library of peptides according to claim 4 32 in such a manner whereby the fluorogenic moiety is released 5 from the peptide sequence, thereby forming a fluorescent moiety;	1	61. A method of determining a peptide sequence specificity profile of
3 (a) contacting said protease with a library of peptides according to claim 4 32 in such a manner whereby the fluorogenic moiety is released 5 from the peptide sequence, thereby forming a fluorescent moiety;		
32 in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;		(a) contacting said protease with a library of peptides according to claim
from the peptide sequence, thereby forming a fluorescent moiety;		32 in such a manner whereby the fluorogenic moiety is released
		from the peptide sequence, thereby forming a fluorescent moiety;
6 (b) detecting said fluorescent molecy,		(b) detecting said fluorescent moiety;
the sequence of said nentide sequence, thereby		
and a consumer specificity profile of said		
9 protease.		

1	62.	The method according to claim 61, further comprising (d)
2	quantifying said fluor	rescent moiety, thereby quantifying said protease.
1	63.	A database comprising at least one set of peptide sequence
2	specificity data for a	protease determined using a library according to claim 32.
1	64.	The database according to claim 63, wherein said database is an
2	electronic database.	
1	65.	The database according to claim 64, wherein said database is
1 2	distributed on a wide	
		A database comprising at least one set of peptide sequence
1	66.	
2	specificity data for a	protease determined using a method according to claim 61.
1	67.	The database according to claim 63, wherein said database is an
2	electronic database.	
1	68.	The database according to claim 64, wherein said database is
2	distributed on a wid	
_		
1	69.	The method according to claim 61, wherein said protease is a
2	member selected from	om the group consisting of aspartic protease, cysteine protease, and
3	serine protease	
1	70.	The method according to claim 61, wherein said protease is a
2	protease of a micro	
_	71	The method according to claim 70, wherein said microorganism is
1	71.	from the group consisting of bacteria, fungi, yeast, viruses, and
2		from the group consisting of bacteria, rungi, years, where,
3	protozoa.	
1	72.	The method according to claim 61, further comprising (c)
2	quantifying the flu	orescent moiety, thereby quantifying said protease.
1	73.	A method of preparing a fluorogenic peptide, said method
1		
2	comprising.	•

(a) providing a first conjugate comprising a fluorogenic moiety covalently bonded
 to a solid support, said conjugate having the structure:

5 wherein, 6 R¹, R², R³, R⁴, R⁵ and R⁶ are members independently selected from the 7 group consisting of H, halogen, -NO2, -CN, 8 $-C(O)_{m}R^{7}, -C(O)NR^{8}R^{9}, -S(O)_{t}R^{10}, -SO_{2}NR^{11}R^{12}, -OR^{13}-NR^{18}R^{19},$ 9 and substituted or unsubstituted alkyl, with the proviso that at least 10 one of R^1 , R^2 , R^3 , R^4 , R^5 and R^6 is $-NH_2$; 11 R^7 , R^8 , R^9 , R^{10} , R^{11} , R^{12} , R^{13} , R^{18} and R^{19} are members 12 independently selected from the group consisting of H, 13 substituted or unsubstituted alkyl and substituted or 14 unsubstituted aryl; 15 m is a member selected from the group consisting of the numbers 16 from 1 to 2; 17 t is a member selected from the group consisting of the numbers 18 from 0 to 2; 19 R⁵ and R⁶ are members independently selected from the group consisting 20 of H and -R¹⁴-C(O)NH-SS, wherein at least one of R⁵ and R⁶ is 21 -R¹⁴-C(O)NH-SS; 22 R¹⁴ is a member selected from the group consisting of substituted 23 or unsubstituted alkyl and substituted or unsubstituted 24 heteroalkyl; 25 SS is a solid support; 26 (b) contacting said first conjugate with a first protected amino acid moiety 27 (pAA1) and an activating agent, thereby forming a peptide bond between a 28 carboxyl group of pAA1 and the aniline nitrogen of said first conjugate; 29 (c) deprotecting said pAA¹, thereby forming a second conjugate having a reactive 30 AA1 amine moiety; 31

32	(d) contacting said second conjugate with a second protected amino acid (pAA ⁻)	
33	and an activating agent, thereby forming a peptide bond between a	
34	carboxyl group of pAA2 and said reactive AA ¹ amine moiety; and	
35	(e) deprotecting said pAA ² , thereby forming a third conjugate having a reactive	
36	AA ² amine moiety.	
1	74. The method according to claim 73, further comprising:	
	(f) contacting said third conjugate with a third protected amino acid (pAA ³) and	
2	an activating agent, thereby forming a peptide bond between a carboxyl	
<i>3</i>	group of pAA ³ and said reactive AA ² amine moiety; and	
5	(e) deprotecting said pAA ³ , thereby forming a fourth conjugate having a reactive	
6	AA ³ amine moiety.	
1	75. The method according to claim 73, further comprising between	
2	steps (b) and (c) capping aniline amine groups that have not reacted with pAA ¹ .	
1	76. The method according to claim 75, wherein said capping utilizes a	
2	mixture comprising an active ester of a carboxylic acid.	
1	77. The method according to claim 78, wherein said active ester is the	
2	nitrotriazole ester of acetic acid.	
1	78. The method according to claim 74, wherein a member selected	
2	from the group consisting of pAA ¹ , pAA ² , pAA ³ and combinations thereof comprises a	
3	mixture of protected amino acids differing in the identity of the amino acid portion of the	
4	protected amino acids.	
1	79. The method according to claim 78, wherein said mixture comprises	
2	at least 2 unique amino acids.	
1	80. The method according to claim 79, wherein said mixture comprises	
2	at least 6 unique amino acids.	
1	81. The method according to claim 80, wherein said mixture comprises	
2	at least 12 unique amino acids.	

- 1 82. The method according to claim 81, wherein said mixture comprises 2 at least 20 unique amino acids.
- 1 83. The method according to claim 78, wherein said mixture is an
- 2 isokinetic mixture.